

## **SEQUENCE LISTING**

<110> C. Frank Bennett  
Nicholas M. Dean  
Lex M. Cowser

## <12.0> ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION

<130> RTS-0066

^160> 182

4210> 1

401 > 20

<212> DNA

*1.000* ±

20

2210

• 2113 20

1123 DNA

### **s313> Artificial Sequence**

#### 1123> Antisense Oligonucleotide

• 100 •

#### REFERENCES AND NOTES

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<212> DNA

Ergonomics in Design

<222> (207), . . . (3668)



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Phe Lys Glu Ala Lys Ile Glu Glu His Leu Ala Arg Val Glu Ala Val  
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Leu Ile Phe Ala Thr Lys Gln Ala Trp Arg Asn Ala Pro Arg Cys Ile  
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Arg Ser Asp Gly Lys His Asp Phe Arg Val Trp Asn Ala Gln Leu Ile  
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Val Leu Phe Ala Cys Met Leu Met Arg Lys Thr Met Ala Ser Arg Val  
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Val Cys Met Asp Lys Tyr Arg Leu Ser Cys Leu Glu Glu Arg Leu  
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His Leu Thr Val Ala Val Val Thr Tyr His Thr Gly Asp Gly Gln Gly  
925 930 935

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Pro Leu His His Gly Val Cys Ser Thr Trp Leu Asn Ser Leu Lys Pro  
940 945 950

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955 960 965

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• 213 • *Mus musculus*

- 22 -

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Met Ala Cys Pro Trp Lys Phe Leu Phe  
1 5  
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Asn Asn Val Glu Lys Ala Pro Cys Ala Thr Ser Ser Pro Val Thr Gln  
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Asp Asp Leu Gln Tyr His Asn Leu Ser Lys Gln Gln Asn Glu Ser Pro  
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60 65 70  
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Leu Asp Ala Thr Pro Leu Ser Ser Pro Arg His Val Arg Ile Lys Asn  
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Trp Gly Ser Gly Met Thr Phe Gln Asp Thr Leu His His Lys Ala Lys  
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ggg att tta act tgc agg tcc aaa tct tgc ctg ggg tcc att atg act 569  
Gly Ile Leu Thr Cys Arg Ser Lys Ser Cys Leu Gly Ser Ile Met Thr  
110 115 120  
ccc aaa agt ttc acc aca gca ccc agg gac aag cct acc cct cca dat 617  
Pro Lys Ser Leu Thr Arg Gly Pro Arg Asp Lys Pro Thr Pro Pro Asp  
125 130 135  
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210		215	
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635	640	645	
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gag gac gcc ttc cgc agc tgg gcc gtg caa acc ttc aag gca gcc tgt Glu Asp Ala Phe Arg Ser Tri Ala Val Gln Thr Phe Lys Ala Ala Cys			2249
670	675	680	

685	690	695	
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ccg aca tcc agc cgt gcc acc atc ctg gtg gaa ctc tcc tgt gag gat Pro Thr Ser Ser Arg Ala Thr Ile Leu Val Glu Leu Ser Cys Glu Asp 750	755	760	2489
ggc caa ggc ctg aac tac ctg ccg ggg gag cac ctt ggg gtt tgc cca Gly Gln Gly Leu Asn Tyr Leu Pro Gly Glu His Leu Gly Val Cys Pro 765	770	775	2537
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ggc ccc aca ccc cac cag aca gtg cgc ctg gag gac ctg gat gag agt Gly Pro Thr Pro His Gln Thr Val Arg Leu Glu Asp Leu Asp Glu Ser 795	800	805	2633
ggc agc tac tgg gtc agt gac aag agg ctg ccc tgc tca ctc agc Gly Ser Tyr Trp Val Ser Asp Lys Arg Leu Pro Pro Cys Ser Leu Ser 810	815	820	825
cag gcc ctc acc tac tcc ccg gac atc acc aca ccc cca acc caq ctg Gln Ala Leu Thr Tyr Ser Pro Asp Ile Thr Pro Pro Thr Gln Leu 830	835	840	2729
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860	865	870	
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875	880	885	
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925	930	935	
ccc ctg cac cac ggt gtc tgc agc aca tgg ctc aac agc ctg aag ccc Pro Leu His His Gly Val Cys Ser Thr Trp Leu Asn Ser Leu Lys Pro			3065
940	945	950	
caa gac cca gtg ccc tgc ttt gtg cggtt aat gcc agc gcc ttc cac ctc Gln Asp Pro Val Pro Cys Phe Val Arg Asn Ala Ser Ala Phe His Leu			3113
955	960	965	
ccc gag gat ccc tcc cat cct tgc atc ctc atc ggg cct ggc aca ggc Pro Glu Asp Pro Ser His Pro Cys Ile Leu Ile Gly Pro Gly Thr Gly			3161
970	975	980	985
atc gtg ccc ttc cgc agt ttc tgg cag caa cggtt ctc cat gac tcc cag Ile Val Pro Phe Arg Ser Phe Trp Gln Gln Arg Leu His Asp Ser Gln			3209
990	995	1000	
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1005	1010	1015	
cgcc cca gat gag gac cac atc tac cag gag gag atg ctg gag atg gcc Arg Pro Asp Glu Asp His Ile Tyr Gln Glu Glu Met Leu Glu Met Ala			3305
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1035	1040	1045	
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1050	1055	1060	1065
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1070	1075	1080	
tgc ggg gat gtg cgc atg gcc cgg gac gtg gcc cac acc ctg aag cag Cys Gly Asp Val Arg Met Ala Arg Asp Val Ala His Thr Leu Lys Gln			3497
1085	1090	1095	
ctg gtg gct gcc aag ctg aaa ttg aat gag gag cag gtc gag gac tat Leu Val Ala Ala Lys Leu Lys Leu Asn Glu Glu Gln Val Glu Asp Tyr			3545
1100	1105	1110	
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1115	1120	1125	
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1130	1135	1140	1145
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a<sup>+</sup>ggagatat ttacatgaat tgcattttac tttaatc

4145

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23

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22

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26

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20

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20

&lt;210&gt; 16

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;223&gt; PCR Probe

&lt;400&gt; 16

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27

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;221&gt; CDS

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1

5

54

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Trp Val Trp Val Ser Leu Leu Val Ala Ala Gly Thr Val Gln Pro Ser

102

Asp Ser Gln Ser Val Cys Ala Gly Thr Glu Asn Lys Leu Ser Ser Leu  
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tct gac ctg gaa cag cag tac cga gcc ttg cgc aag tac tat gaa aac 198  
Ser Asp Leu Glu Gln Gln Tyr Arg Ala Leu Arg Lys Tyr Tyr Glu Asn  
40 45 50 55

tgt gag gtt gtc atg ggc aac ctg gag ata acc agc att gag cac aac 246  
Cys Glu Val Val Met Gly Asn Leu Glu Ile Thr Ser Ile Glu His Asn  
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cgg gac ctc tcc ttc ctg cgg tct gtt cga gaa gtc aca ggc tac gtg 294  
Arg Asp Leu Ser Phe Leu Arg Ser Val Arg Glu Val Thr Gly Tyr Val  
75 80 85

tta gtg gct ctt aat cag ttt cat tac ctg cct ctg gag aat tta cgc 342  
Leu Val Ala Leu Asn Gln Phe Arg Tyr Leu Pro Leu Glu Asn Leu Arg  
90 95 100

att att cgt ggg aca aaa ctt tat gag gat cga tat gcc ttg gca ata 390  
Ile Ile Arg Gly Thr Lys Leu Tyr Glu Asp Arg Tyr Ala Leu Ala Ile  
105 110 115

ttt tta aac tac aga aaa gat gga aac ttt gga ctt caa gaa ctt gga 438  
Phe Leu Asn Tyr Arg Lys Asp Gly Asn Phe Gly Leu Gln Glu Leu Gly  
120 125 130 135

tta aag aac ttg aca gaa atc cta aat ggt gga gtc tat gta gac cag 486  
Leu Lys Asn Leu Thr Glu Ile Leu Asn Gly Gly Val Tyr Val Asp Gln  
140 145 150

aac aaa ttc ctt tgt tat gca gac acc att cat tgg caa gat att gtt 534  
Asn Lys Phe Leu Cys Tyr Ala Asp Thr Ile His Trp Gln Asp Ile Val  
155 160 165

cggtt aac tgg cct tcc aac ttg act ctt gtg tca aca aat ggt aqt 582  
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170 175 180

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Ser Asn Cys Asn Asn Cys Ile Ser Ser Cys Thr Gly Arg Cys Trp Gly

Pro Thr Glu Asn His Cys Gln Thr Leu Thr Arg Thr Val Cys Ala Glu  
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250 255 260

caa acc ttt gtc tac aat cca acc acc ttt caa ctg gag cac aat ttc 870  
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265 270 275

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280 285 290 295

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300 305 310

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315 320 325

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Asp Ile Cys Pro Lys Ala Cys Asp Gly Ile Gly Thr Gly Ser Leu Met  
330 335 340

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Ser Ala Gln Thr Val Asp Ser Ser Asn Ile Asp Lys Phe Ile Asn Cys  
345 350 355

acc aag atc aat ggg aat ttg atc ttt cta gtc act gat att cat ggg 1158  
and the like amino acids from the phe leu val thr gly ile his gly

Asp Pro Tyr Asn Ala Ile Glu Ala Ile Asp Pro Glu Lys Leu Asn Val  
380 385 390

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Phe Arg Thr Val Arg Glu Ile Thr Gly Phe Leu Asn Ile Gln Ser Trp  
395 400 405

cca cca aac atg act gac ttc agt gtt ttt tct aac ctg gtg acc att 1302  
Pro Pro Asn Met Thr Asp Phe Ser Val Phe Ser Asn Leu Val Thr Ile  
410 415 420

ggt gga aga gta ctc tat agt ggc ctg tcc ttg ctt atc ctc aag caa 1350  
Gly Gly Arg Val Leu Tyr Ser Gly Leu Ser Leu Leu Ile Leu Lys Gln  
425 430 435

cag ggc atc acc tct cta cag ttc cag tcc ctg aag gaa atc agc gca 1398  
Gln Gly Ile Thr Ser Leu Gln Phe Gln Ser Leu Lys Glu Ile Ser Ala  
440 445 450 455

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Gly Asn Ile Tyr Ile Thr Asp Asn Ser Asn Leu Cys Tyr Tyr His Thr  
460 465 470

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Ile Asn Trp Thr Thr Leu Phe Ser Thr Ile Asn Gln Arg Ile Val Ile  
475 480 485

cgg gac aac aga aaa gct gaa aat tgt act gct gaa gga atg gtg tgc 1542  
Arg Asp Asn Arg Lys Ala Glu Asn Cys Thr Ala Glu Gly Met Val Cys  
490 495 500

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505 510 515

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Cys Leu Ser Cys Arg Arg Phe Ser Arg Gly Arg Ile Cys Ile Glu Ser  
520 525 530 535

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Cys Asn Leu Tyr Asp Gly Glu Phe Arg Glu Phe Glu Asn Gly Ser Ile

Cys Val Glu Cys Asp Pro Gln Cys Glu Lys Met Glu Asp Gly Leu Leu  
555 560 565  
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Thr Cys His Gly Pro Gly Pro Asp Asn Cys Thr Lys Cys Ser His Phe  
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Lys Asp Gly Pro Asn Cys Val Glu Lys Cys Pro Asp Gly Leu Gln Gly  
585 590 595  
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 Val Lys Ile Pro Val Ala Ile Lys Ile Leu Asn Glu Thr Thr Gly Pro  
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 Lys Ala Asn Val Glu Phe Met Asp Glu Ala Leu Ile Met Ala Ser Met  
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 Asp His Pro His Leu Val Arg Leu Leu Gly Val Cys Leu Ser Pro Thr  
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 Ile Gln Leu Val Thr Gln Leu Met Pro His Gly Cys Leu Leu Glu Tyr  
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 Val His Glu His Lys Asp Asn Ile Gly Ser Gln Leu Leu Asn Trp  
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 tgt gtc cag ata gct aag gga atg atg tac ctg gaa gaa aga cga ctc 2550  
 Cys Val Gln Ile Ala Lys Gly Met Met Tyr Leu Glu Glu Arg Arg Leu  
 825 830 835  
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 Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Ser Pro Asn  
 840 845 850 855  
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 His Val Lys Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu Glu Gly Asp  
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 Glu Lys Glu Tyr Asn Ala Asp Gly Gly Lys Met Pro Ile Lys Trp Met  
 875 880 885  
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 Ser Lys Glu Cys Tyr Asn Ala Asp Phe Thr His Gln Ser Asp Val

Trp Ser Tyr Gly Val Thr Ile Trp Glu Leu Met Thr Phe Gly Gly Lys  
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Val Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe  
955 960 965

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Ile Gly His Ser Pro Pro Ala Tyr Thr Pro Met Ser Gly Asn Gln  
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aag aaa acc cct tgt gct gtt ctc agc cca aca ata caa gat gac cct Lys Lys Thr Pro Cys Ala Val Leu Ser Pro Thr Ile Gln Asp Asp Pro	30	35	40	387
aag agt cac caa aat ggc tcc ccg cag ctc ctc act ggg aca gca cag Lys Ser His Gln Asn Gly Ser Pro Gln Leu Leu Thr Gly Thr Ala Gln	45	50	55	435
aat gtt cca gaa tcc ctg gac aag ctg cat gtg aca tcg acc cgt cca Asn Val Pro Glu Ser Leu Asp Lys Leu His Val Thr Ser Thr Arg Pro	65	70	75	483
cag tat gtg agg atc aaa aac tgg ggc agt gga gag att ttg cat gac Gln Tyr Val Arg Ile Lys Asn Trp Gly Ser Gly Glu Ile Leu His Asp	80	85	90	531
act ctt cac cac aag gcc aca tcg gat ttc act tgc aag tcc aag tct Thr Leu His His Lys Ala Thr Ser Asp Phe Thr Cys Lys Ser Lys Ser	95	100	105	579
tgc ttg ggg tcc atc atg aac ccc aag agt ttg acc aga gga ccc aga Cys Leu Gly Ser Ile Met Asn Pro Lys Ser Leu Thr Arg Gly Pro Arg	110	115	120	627
gac aag cct acc cct ctg gag gag ctc ctg cct cat gcc att gag ttc Asp Lys Pro Thr Pro Leu Glu Leu Leu Pro His Ala Ile Glu Phe	125	130	135	675
atc aac cag tat tat ggc tcc ttt aaa gag gca aaa ata gag gaa cat Ile Asn Gln Tyr Tyr Gly Ser Phe Lys Glu Ala Lys Ile Glu Glu His	145	150	155	723
ctg gcc agg ctg gaa gct gta aca aag gaa ata gaa aca aca gga acc Leu Ala Arg Leu Glu Ala Val Thr Lys Glu Ile Glu Thr Thr Gly Thr	160	165	170	771

agg aat gcc cct cgc tgc atc ggc agg atc cag tgg tcc aac ctg cag 867  
Arg Asn Ala Pro Arg Cys Ile Gly Arg Ile Gln Trp Ser Asn Leu Gln  
190 195 200

gtc ttt gac gct cgg aac tgt agc aca gca cag gaa atg ttt cag cac 915  
Val Phe Asp Ala Arg Asn Cys Ser Thr Ala Gln Glu Met Phe Gln His  
205 210 215 220

atc tgc aga cac ata ctt tat gcc acc aac aat ggc aac atc agg tcg 963  
Ile Cys Arg His Ile Leu Tyr Ala Thr Asn Asn Gly Asn Ile Arg Ser  
225 230 235

gcc atc act gtg ttc ccc cag cgg agt gac ggc aaa cat gac ttc agg 1011  
Ala Ile Thr Val Phe Pro Gln Arg Ser Asp Gly Lys His Asp Phe Arg  
240 245 250

ctc tgg aat tca cag ctc atc cgg tac gct ggc tac cag atg ccc gat 1059  
Leu Trp Asn Ser Gln Leu Ile Arg Tyr Ala Gly Tyr Gln Met Pro Asp  
255 260 265

ggc acc atc aga ggg gat gct gcc acc ttg gag ttc acc cag ttg tgc 1107  
Gly Thr Ile Arg Gly Asp Ala Ala Thr Leu Glu Phe Thr Gln Leu Cys  
270 275 280

atc gac cta ggc tgg aag ccc cgc tat ggc cgc ttt gat gtg ctg cct 1155  
Ile Asp Leu Gly Trp Lys Pro Arg Tyr Gly Arg Phe Asp Val Leu Pro  
285 290 295 300

ctg gtc ttg caa gct gat ggt caa gat cca gag gtc ttt gaa atc cct 1203  
Leu Val Leu Gln Ala Asp Gly Gln Asp Pro Glu Val Phe Glu Ile Pro  
305 310 315

cct gat ctt gtg ttg gag gtg acc atg gag cat ccc aag tac gag tgg 1251  
Pro Asp Leu Val Leu Glu Val Thr Met Glu His Pro Lys Tyr Glu Trp  
320 325 330

ttc cag gag ctc ggg ttg aag tgg tat gca ctg cct gcc gtg gcc aac 1299  
Phe Gln Glu Leu Gly Leu Lys Trp Tyr Ala Leu Pro Ala Val Ala Asn  
335 340 345

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Leu Val Leu Glu Val Thr Met Glu His Pro Lys Tyr Glu Trp

ggt tgg tac atg ggc acc gag att gga gtt cga gac ttc tgt gac aca Gly Trp Tyr Met Gly Thr Glu Ile Gly Val Arg Asp Phe Cys Asp Thr	365	370	375	380	1395
cag cgc tac aac atc ctg gag gaa gtg ggc cga agg atg ggc ctg gag Gln Arg Tyr Asn Ile Leu Glu Glu Val Gly Arg Arg Met Gly Leu Glu	385		390	395	1443
acc cac aca ctg gcc tcc ctc tgg aaa gac cgg gct gtc acg gag atc Thr His Thr Leu Ala Ser Leu Trp Lys Asp Arg Ala Val Thr Glu Ile	400		405	410	1491
aat gtg gct gtg ctc cat agt ttc cag aag cag aat gtg acc atc atg Asn Val Ala Val Leu His Ser Phe Gln Lys Gln Asn Val Thr Ile Met	415		420	425	1539
gac cac cac aca gcc tca gag tcc ttc atg aag cac atg cag aat gag Asp His His Thr Ala Ser Glu Ser Phe Met Lys His Met Gln Asn Glu	430		435	440	1587
tac cgg gcc cgt gga ggc tgc ccg gca gac tgg att tgg ctg gtc cct Tyr Arg Ala Arg Gly Gly Cys Pro Ala Asp Trp Ile Trp Leu Val Pro	445		450	455	1635
445		450	455	460	
cca gtg tct ggg agc atc acc cct gtg ttc cac cag gag atg ttg aac Pro Val Ser Gly Ser Ile Thr Pro Val Phe His Gln Glu Met Leu Asn	465		470	475	1683
465		470	475		
tat gtc cta tct cca ttc tac tac tac cag atc gag ccc tgg aag acc Tyr Val Leu Ser Pro Phe Tyr Tyr Gln Ile Glu Pro Trp Lys Thr	480		485	490	1731
480		485	490		
cac atc tgg cag aat gag aag ctg agg ccc agg agg aga gag atc cga His Ile Trp Gln Asn Glu Lys Leu Arg Pro Arg Arg Arg Glu Ile Arg	495		500	505	1779
495		500	505		
ttt aga gtc ttg gtg aaa gtg gtg ttc ttt gct tcc atg cta atg cga Phe Arg Val Leu Val Lys Val Val Phe Phe Ala Ser Met Leu Met Arg	510		515	520	1827
510		515	520		

aca ggg aag tct gaa gca cta gcc agg gac ctg gcc acc ttg ttc agc 1923  
 Thr Gly Lys Ser Glu Ala Leu Ala Arg Asp Leu Ala Thr Leu Phe Ser  
       545                  550                  555  
  
 tac gcc ttc aac acc aag gtt gtc tgc atg gac cag tat aag gca agc 1971  
 Tyr Ala Phe Asn Thr Lys Val Val Cys Met Asp Gln Tyr Lys Ala Ser  
       560                  565                  570  
  
 acc ttg gaa gag gag caa cta ctg ctg gtg aca agc aca ttt ggg 2019  
 Thr Leu Glu Glu Gln Leu Leu Val Val Thr Ser Thr Phe Gly  
       575                  580                  585  
  
 aat gga gac tgt ccc agc aat ggg cag act ctg aag aaa tct ctg ttc 2067  
 Asn Gly Asp Cys Pro Ser Asn Gly Gln Thr Leu Lys Ser Leu Phe  
       590                  595                  600  
  
 atg ctt aga gaa ctc aac cac acc ttc agg tat gct gtg ttt ggc ctt 2115  
 Met Leu Arg Glu Leu Asn His Thr Phe Arg Tyr Ala Val Phe Gly Leu  
       605                  610                  615                  620  
  
 ggc tcc agc atg tac cct cag ttc tgc gcc ttt gct cat gac atc gac 2163  
 Gly Ser Ser Met Tyr Pro Gln Phe Cys Ala Phe Ala His Asp Ile Asp  
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 Gln Lys Leu Ser His Leu Gly Ala Ser Gln Leu Ala Pro Thr Gly Glu  
       640                  645                  650  
  
 ggg gac gaa ctc agt ggg cag gag gat gcc ttc cgc agc tgg gct gta 2259  
 Gly Asp Glu Leu Ser Gly Gln Glu Asp Ala Phe Arg Ser Trp Ala Val  
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 caa acc ttc cgg gca gcc tgt gag acc ttt gat gtc cga agc aaa cat 2307  
 Gln Thr Phe Arg Ala Ala Cys Glu Thr Phe Asp Val Arg Ser Lys His  
       670                  675                  680  
  
 cac att cag atc ccg aaa cgc ttc act tcc aat gca aca tgg gag cca 2355  
 His Ile Gln Ile Pro Lys Arg Phe Thr Ser Asn Ala Thr Trp Glu Pro  
       685                  690                  695                  700  
  
 caa caa tat aag ctc atc caq aqc ccg qaq cct tta gac ctc aac aga 2403

gcc ctc agc agc atc cat gca aag aac gtg ttt acc atg agg ctg aaa 2451  
Ala Leu Ser Ser Ile His Ala Lys Asn Val Phe Thr Met Arg Leu Lys  
720 725 730

tcc cag cag aat ctg cag agt gaa aag tcc agc cgc acc acc ctc ctc 2499  
Ser Gln Gln Asn Leu Gln Ser Glu Lys Ser Ser Arg Thr Thr Leu Leu  
735 740 745

gtt cag ctc acc ttc gag ggc agc cga ggg ccc agc tac ctg cct ggg 2547  
Val Gln Leu Thr Phe Glu Gly Ser Arg Gly Pro Ser Tyr Leu Pro Gly  
750 755 760

gaa cac ctg ggg atc ttc cca ggc aac cag acc gcc ctg gtg cag gga 2595  
Glu His Leu Gly Ile Phe Pro Gly Asn Gln Thr Ala Leu Val Gln Gly  
765 770 775 780

atc ttg gag cga gtt gtg gat tgt cct aca cca cac caa act gtg tgc 2643  
Ile Leu Glu Arg Val Val Asp Cys Pro Thr Pro His Gln Thr Val Cys  
785 790 795

ctg gag gtt ctg gat gag agc ggc agc tac tgg gtc aaa gac aag agg 2691  
Leu Glu Val Leu Asp Glu Ser Gly Ser Tyr Trp Val Lys Asp Lys Arg  
800 805 810

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Leu Pro Pro Cys Ser Leu Ser Gln Ala Leu Thr Tyr Phe Leu Asp Ile  
815 820 825

acg acc cct ccc acc cag ctg cag ctc cac aag ctg gct cgc ttt gcc 2787  
Thr Thr Pro Pro Thr Gln Leu Gln Leu His Lys Leu Ala Arg Phe Ala  
830 835 840

acg gac gag acg gat agg cag aga ttg gag gcc ttg tgt cag ccc tca 2835  
Thr Asp Glu Thr Asp Arg Gln Arg Leu Glu Ala Leu Cys Gln Pro Ser  
845 850 855 860

gag tac aat gac tgg aag ttc agc aac ccc acg ttc ctg gag gtg 2883  
Glu Tyr Asn Asp Trp Lys Phe Ser Asn Asn Pro Thr Phe Leu Glu Val  
865 870 875

att aat ctc ctc ctc ttc cat atc ccc act gcc ttc cta cta tca 2931

cag ctc cct atc ttg aag ccc cgc tac tac tcc atc agc tcc tcc cag Gln Leu Pro Ile Leu Lys Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Gln	895	900	905	2979
gac cac acc ccc tcg gag gtt cac ctc act gtg gcc gtg gtc acc tac Asp His Thr Pro Ser Glu Val His Leu Thr Val Ala Val Val Thr Tyr	910	915	920	3027
cgc acc cga gat ggt cag ggt ccc ctg cac cat ggt gtc tgc agc act Arg Thr Arg Asp Gly Gln Gly Pro Leu His His Gly Val Cys Ser Thr	925	930	935	3075
tgg atc agg aac ctg aag ccc cag gac cca gtg ccc tgc ttt gtg cga Trp Ile Arg Asn Leu Lys Pro Gln Asp Pro Val Pro Cys Phe Val Arg	945	950	955	3123
agt gtc agt ggc ttc cag ctc cct gag gac ccc tcc cag cct tgc atc Ser Val Ser Gly Phe Gln Leu Pro Glu Asp Pro Ser Gln Pro Cys Ile	960	965	970	3171
ctc att ggg cct ggt acg ggc att gct ccc ttc cga agt ttc tgg cag Leu Ile Gly Pro Gly Thr Gly Ile Ala Pro Phe Arg Ser Phe Trp Gln	975	980	985	3219
cag cgg ctc cat gac tcc cag cac aaa ggg ctc aaa gga ggc cgc atg Gln Arg Leu His Asp Ser Gln His Lys Gly Leu Lys Gly Gly Arg Met	990	995	1000	3267
agc ttg gtg ttt ggg tgc cgg cac ccg gag gag gac cac ctc tat cag Ser Leu Val Phe Gly Cys Arg His Pro Glu Glu Asp His Leu Tyr Gln	1005	1010	1015	3315
gaa gaa atq cag qaq atq gtc cgc aag aga gtq ctg ttc cag gtg cac Glu Glu Met Gln Glu Met Val Arg Lys Arg Val Leu Phe Gln Val His	1025	1030	1035	3363
aca ggc tac tcc cgg ctg ccc ggc aaa ccc aag gtc tac gtt cag gac Thr Gly Tyr Ser Arg Leu Pro Gly Lys Pro Lys Val Tyr Val Gln Asp	1040	1045	1050	3411
3459				

gag cag ggc cac ctc tac att tgc gga gat gtg cgc atg gct cgg gat 3507  
 Glu Gln Gly His Leu Tyr Ile Cys Gly Asp Val Arg Met Ala Arg Asp  
 1070 1075 1080

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gtg gct acc aca ttg aag aag ctg gtg gcc acc aag ctg aac ttg agc      3555
Val Ala Thr Thr Leu Lys Lys Leu Val Ala Thr Lys Leu Asn Leu Ser
1085           1090           1095           1100

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gag gag cag gtg gaa gac tat ttc ttc cag ctc aag agc cag aaa cgt 3603  
 Glu Glu Gln Val Glu Asp Tyr Phe Phe Gln Leu Lys Ser Gln Lys Arg  
 1105 1110 1115

tat cat gaa gat atc ttc ggt gca gtc ttt tcc tat ggg gca aaa aag 3651  
 Tyr His Glu Asp Ile Phe Gly Ala Val Phe Ser Tyr Gly Ala Lys Lys  
 1120 1125 1130

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• 211 • 18

1112 • J. Neurosci., April 1, 1998

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estimated error  $\pm 1\%$

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• 106

• 118

#### 3.12.2. rDNAs

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• 100 • 6

at [taggit](#)

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 $\sim 270000 \times 10^3$

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18

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18

&lt;210&gt; 79

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ggcaaaggcag tctgtgtc

18

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